

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: YISSUM RES. DEV. CO. OF THE HEBREW UNIV. OF JERUSALEM
- (B) STREET: 46 Jabotinsky
- (C) CITY: Jerusalem
- (E) COUNTRY: ISRAEL
- (F) POSTAL CODE (ZIP): 91042
- (G) TELEPHONE: 972-2-5634880
- (H) TELEFAX: 972-2-5660331

(ii) TITLE OF INVENTION: BROAD SPECTRUM PEPTIDE ANTAGONISTS

(iii) NUMBER OF SEQUENCES: 12

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu Asp  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Lys Lys Lys Ala Thr Val Gln Glu Leu Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Lys Lys Lys Val Thr Ala Gln Glu Leu Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /label= X  
/note= "N-lauryl cysteine residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Xaa Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu Asp

1

5

10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= X  
/note= "N-lauryl cysteine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys  
1 5 10 15

Lys Ala Thr Val Gln Glu Leu Asp  
20

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys  
1 5 10 15  
Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys Lys Ala Thr Val  
20 25 30  
Glu Leu Asp  
35

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 1..14
- (D) OTHER INFORMATION: /label= X  
/note= "Disulfide bond formed by the two external  
Cys residues."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /label= X  
/note= "Extension with a cysteine residue."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= X  
/note= "Extension with a cysteine residue."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 1  
(D) OTHER INFORMATION: /label= X  
/note= "D-alanine residue."

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 14  
(D) OTHER INFORMATION: /label= X  
/note= "D-alanine residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /label= X  
/note= "N-acetyl group"

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 14  
(D) OTHER INFORMATION: /label= X  
/note= "D-alanine residue."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 239 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Staphylococcus aureus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Glu	Ser	Gln	Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys	Ser	Ser	Lys	1	5	10	15
Phe	Thr	Gly	Leu	Met	Glu	Asn	Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	20	25	30	
Val	Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln	Phe	Leu	Tyr	Phe	Asp	35	40	45	
Leu	Ile	Tyr	Ser	Ile	Lys	Asp	Thr	Lys	Leu	Gly	Asn	Tyr	Asp	Asn	Val	50	55	60	
Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu	Ala	Asp	Lys	Tyr	Lys	Asp	Lys	65	70	75	80
Tyr	Val	Asp	Val	Phe	Gly	Ala	Asn	Tyr	Tyr	Tyr	Gln	Cys	Tyr	Phe	Ser	85	90	95	
Lys	Lys	Thr	Asn	Asp	Ile	Asn	Ser	His	Glu	Thr	Asp	Lys	Arg	Lys	Thr	100	105	110	
Cys	Met	Tyr	Gly	Gly	Val	Thr	Glu	His	Asn	Gly	Asn	Gln	Leu	Asp	Lys	115	120	125	
Tyr	Arg	Ser	Ile	Thr	Val	Arg	Val	Phe	Glu	Asp	Gly	Lys	Asn	Leu	Leu	130	135	140	
Ser	Phe	Asp	Val	Gln	Thr	Asn	Lys	Lys	Lys	Val	Thr	Ala	Gln	Glu	Leu	145	150	155	160
Asp	Tyr	Leu	Thr	Arg	His	Tyr	Leu	Val	Lys	Asn	Lys	Lys	Leu	Tyr	Glu	165	170	175	
Phe	Asn	Asn	Ser	Pro	Tyr	Glu	Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	180	185	190	
Glu	Asn	Ser	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala	Pro	Gly	Asp	Lys	Phe	195	200	205	
Asp	Gln	Ser	Lys	Tyr	Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Met	Val	Asp	210	215	220	
Ser	Lys	Asp	Val	Lys	Ile	Glu	Val	Tyr	Leu	Thr	Thr	Lys	Lys	Lys	225	230	235		